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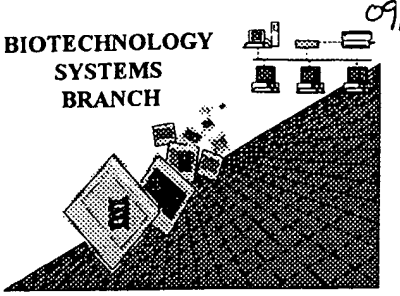
#4/24
09/07

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: ~~09/292,436~~ 09/292,437

Art Unit / Team No. : OIPE

Date Processed by STIC: 4/28/99 GAU 1643

This paper was misfiled.

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

This Raw Listing contains the General Information Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

<110> APPLICANT: Olaf Schneewind
Sarkis Mazmanian
Gwen Liu
Hung Ton-That
<120> TITLE OF INVENTION: IDENTIFICATION OF SORTASE GENE
<130> FILE REFERENCE: 510015.213
<140> CURRENT APPLICATION NUMBER: ~~US/09/292,436~~ 09/292,437
<141> CURRENT FILING DATE: 1999-04-15
<160> NUMBER OF SEQ ID NOS: 36
<170> SOFTWARE: FastSEQ for Windows Version 3.0
<210> SEQ ID NO 1
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Bacteria
<400> SEQUENCE: 1
W--> Leu Pro Xaa Thr Gly
1 5

see item 10 on Cover Summary Sheet

<210> SEQ ID NO 2
<211> LENGTH: 621
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(621)
<400> SEQUENCE: 2

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atg aaa aaa tgg aca aat cga tta atg aca atc gct ggt gtg gta ctt       48
Met Lys Lys Trp Thr Asn Arg Leu Met Thr Ile Ala Gly Val Val Leu
 1               5                  10                  15
atc cta gtg gca gca tat ttg ttt gct aaa cca cat atc gat aat tat       96
Ile Leu Val Ala Ala Tyr Leu Phe Ala Lys Pro His Ile Asp Asn Tyr
            20                  25                  30
ctt cac gat aaa gat aaa gat gaa aag att gaa caa tat gat aaa aat      144
Leu His Asp Lys Asp Lys Asp Glu Lys Ile Glu Gln Tyr Asp Lys Asn
        35                  40                  45
gta aaa gaa cag gcg agt aaa gat aaa aag cag caa gct aaa cct caa      192
Val Lys Glu Gln Ala Ser Lys Asp Lys Lys Gln Gln Ala Lys Pro Gln
    50                  55                  60
att ccg aaa gat aaa tcg aaa gtg gca ggc tat att gaa att cca gat      240
Ile Pro Lys Asp Lys Ser Lys Val Ala Gly Tyr Ile Glu Ile Pro Asp
65                  70                  75                  80
gct gat att aaa gaa cca gta tat cca gga cca gca aca cct gaa caa      288
Ala Asp Ile Lys Glu Pro Val Tyr Pro Gly Pro Ala Thr Pro Glu Gln
                85                  90                  95
tta aat aga ggt gta agc ttt gca gaa gaa aat gaa tca cta gat gat      336
```

```
45          Leu Asn Arg Gly Val Ser Phe Ala Glu Glu Asn Glu Ser Leu Asp Asp
46                      100                 105                 110
47          caa aat att tca att gca gga cac act ttc att gac cgt ccg aac tat      384
48          Gln Asn Ile Ser Ile Ala Gly His Thr Phe Ile Asp Arg Pro Asn Tyr
49                  115                 120                 125
50          caa ttt aca aat ctt aaa gca gcc aaa aaa ggt agt atg gtg tac ttt      432
51          Gln Phe Thr Asn Leu Lys Ala Ala Lys Lys Gly Ser Met Val Tyr Phe
52              130                 135                 140
53          aaa gtt ggt aat gaa aca cgt aag tat aaa atg aca agt ata aga gat      480
54          Lys Val Gly Asn Glu Thr Arg Lys Tyr Lys Met Thr Ser Ile Arg Asp
55          145                 150                 155                 160
56          gtt aag cct aca gat gta gga gtt cta gat gaa caa aaa ggt aaa gat      528
57          Val Lys Pro Thr Asp Val Gly Val Leu Asp Glu Gln Lys Gly Lys Asp
58                          165                 170                 175
59          aaa caa tta aca tta att act tgt gat gat tac aat gaa aag aca ggc      576
60          Lys Gln Leu Thr Leu Ile Thr Cys Asp Asp Tyr Asn Glu Lys Thr Gly
61                      180                 185                 190
62          gtt tgg gaa aaa cgt aaa atc ttt gta gct aca gaa gtc aaa taa          621
W--> 63     Val Trp Glu Lys Arg Lys Ile Phe Val Ala Thr Glu Val Lys
64                  195                 200                 205
65  <210> SEQ ID NO 3
66  <211> LENGTH: 206
67  <212> TYPE: PRT
68  <213> ORGANISM: Staphylococcus aureus
69  <400> SEQUENCE: 3
70          Met Lys Lys Trp Thr Asn Arg Leu Met Thr Ile Ala Gly Val Val Leu
71           1               5                  10                  15
72          Ile Leu Val Ala Ala Tyr Leu Phe Ala Lys Pro His Ile Asp Asn Tyr
73                      20                  25                  30
74          Leu His Asp Lys Asp Lys Asp Glu Lys Ile Glu Gln Tyr Asp Lys Asn
75                  35                  40                  45
76          Val Lys Glu Gln Ala Ser Lys Asp Lys Lys Gln Gln Ala Lys Pro Gln
77              50                  55                  60
78          Ile Pro Lys Asp Lys Ser Lys Val Ala Gly Tyr Ile Glu Ile Pro Asp
79          65                  70                  75                  80
80          Ala Asp Ile Lys Glu Pro Val Tyr Pro Gly Pro Ala Thr Pro Glu Gln
81                          85                  90                  95
82          Leu Asn Arg Gly Val Ser Phe Ala Glu Glu Asn Glu Ser Leu Asp Asp
83                      100                 105                 110
84          Gln Asn Ile Ser Ile Ala Gly His Thr Phe Ile Asp Arg Pro Asn Tyr
85                  115                 120                 125
86          Gln Phe Thr Asn Leu Lys Ala Ala Lys Lys Gly Ser Met Val Tyr Phe
87              130                 135                 140
88          Lys Val Gly Asn Glu Thr Arg Lys Tyr Lys Met Thr Ser Ile Arg Asp
89          145                 150                 155                 160
90          Val Lys Pro Thr Asp Val Gly Val Leu Asp Glu Gln Lys Gly Lys Asp
91                          165                 170                 175
92          Lys Gln Leu Thr Leu Ile Thr Cys Asp Asp Tyr Asn Glu Lys Thr Gly
93                      180                 185                 190
94          Val Trp Glu Lys Arg Lys Ile Phe Val Ala Thr Glu Val Lys
```

```
                195                 200                 205

<210> SEQ ID NO 4
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 4
Met Glu Glu Val Trp Gln Lys Ala Lys Ala Tyr Asn Ala Arg Leu Gly
 1               5                  10                  15
Thr Gln Pro Val Pro Asp Ala Phe Ser Phe Arg Asp Gly Ile His Asp
            20                  25                  30
Lys Asn Tyr Glu Ser Leu Leu Gln Ile Glu Asn Asn Asp Ile Met Gly
        35                  40                  45
Tyr Val Glu Val Pro Ser Ile Lys Val Thr Leu Pro Ile Tyr His Tyr
    50                  55                  60
Thr Thr Asp Glu Val Leu Thr Lys Gly Ala Gly His Leu Phe Gly Ser
65                  70                  75                  80
Ala Leu Pro Val Gly Gly Asp Gly Thr His Thr Val Ile Ser Ala His
                85                  90                  95
Arg Gly Leu Pro Ser Ala Glu Met Phe Thr Asn Leu Asn Leu Val Lys
            100                 105                 110
Lys Gly Asp Thr Phe Tyr Phe Arg Val Leu Asn Lys Val Leu Ala Tyr
        115                 120                 125
Lys Val Asp Gln Ile Leu Thr Val Glu Pro Asp Gln Val Thr Ser Leu
    130                 135                 140
Ser Gly Val Met Gly Lys Asp Tyr Ala Thr Leu Val Thr Cys Thr Pro
145                 150                 155                 160
Tyr Gly Val Asn Thr Lys Arg Leu Leu Val Arg Gly His Arg Ile Ala
                165                 170                 175
Tyr His Tyr Lys Lys Tyr Gln Gln Ala Lys Lys Ala Met Lys Leu Val
            180                 185                 190
Asp Lys Ser Arg Met Trp Ala Glu Val Val Cys Ala Ala Phe Gly Val
        195                 200                 205
Val Ile Ala Ile Ile Leu Val Phe Met Tyr Ser Arg Val Ser Ala Lys
    210                 215                 220
Lys Ser Lys
225

<210> SEQ ID NO 5
<211> LENGTH: 365
<212> TYPE: PRT
<213> ORGANISM: Actinomyces naeslundii
<400> SEQUENCE: 5
Met Gly Leu Leu Thr Tyr Pro Thr Ala Ala Ser Trp Val Ser Gln Tyr
 1               5                  10                  15
Asn Gln Ser Lys Val Thr Ala Asp Tyr Ser Ala Gln Val Asp Gly Ala
            20                  25                  30
Arg Pro Asp Ala Lys Thr Gln Val Glu Gln Ala His Ala Tyr Asn Asp
        35                  40                  45
Ala Leu Ser Ala Gly Ala Val Leu Glu Ala Asn Asn His Val Pro Thr
    50                  55                  60
Gly Ala Gly Ser Ser Lys Asp Ser Ser Leu Gln Tyr Ala Asn Ile Leu
```

```
145         65                  70                  75                  80
146         Lys Ala Asn Asn Glu Gly Leu Met Ala Arg Leu Lys Ile Pro Ser Ile
147                         85                  90                  95
148         Ser Leu Asp Leu Pro Val Tyr His Gly Thr Ala Asp Asp Thr Leu Leu
149                     100                 105                 110
150         Lys Gly Leu Gly His Leu Glu Gly Thr Ser Leu Pro Val Gly Gly Glu
151                 115                 120                 125
152         Gly Thr Arg Ser Val Ile Thr Gly His Arg Gly Leu Ala Glu Ala Thr
153             130                 135                 140
154         Met Phe Thr Asn Leu Asp Lys Val Lys Thr Gly Asp Ser Leu Ile Val
155         145                 150                 155                 160
156         Glu Val Phe Gly Glu Val Leu Thr Tyr Arg Val Thr Ser Thr Lys Val
157                         165                 170                 175
158         Val Glu Pro Glu Glu Thr Glu Ala Leu Arg Val Glu Glu Gly Lys Asp
159                     180                 185                 190
160         Leu Leu Thr Leu Val Thr Cys Thr Pro Leu Gly Ile Asn Thr His Arg
161                 195                 200                 205
162         Ile Leu Leu Thr Gly Glu Arg Ile Tyr Pro Thr Pro Ala Lys Asp Leu
163             210                 215                 220
164         Ala Ala Ala Gly Lys Arg Pro Asp Val Pro His Phe Pro Trp Trp Ala
165         225                 230                 235                 240
166         Val Gly Leu Ala Ala Gly Leu Ile Val Val Gly Leu Tyr Leu Trp Arg
167                         245                 250                 255
168         Ser Gly Tyr Ala Ala Ala Arg Ala Lys Glu Arg Ala Leu Ala Arg Ala
169                     260                 265                 270
170         Arg Ala Ala Gln Glu Glu Pro Gln Pro Gln Thr Trp Ala Glu Gln Met
171                 275                 280                 285
172         Arg Ile Trp Met Asp Asp Asp Ala Gly Val Glu Pro Gln Arg Trp Phe
173             290                 295                 300
174         Thr Asp Leu Pro Val Pro Pro Gln Pro Ser Glu Met Glu Asn Leu Ala
175         305                 310                 315                 320
176         Leu Leu Glu Glu Ile Ala Ser Leu Ser Ala Pro Ser Gly Arg Trp Asp
177                         325                 330                 335
178         Asp Gln Glu Leu Ile Asp Thr Ala Glu Ile Pro Val Leu Asp Ala Thr
179                     340                 345                 350
180         Arg Pro Ser Ala Gly Thr Ser Gly Arg Thr His Arg Leu
181                 355                 360                 365
182   <210> SEQ ID NO 6
183   <211> LENGTH: 284
184   <212> TYPE: PRT
185   <213> ORGANISM: Enterococcus faecalis
186   <400> SEQUENCE: 6
187         Met Lys Ser Lys Lys Lys Arg Arg Ile Ile Asp Gly Phe Met Ile Leu
188          1               5                  10                  15
189         Leu Leu Ile Ile Gly Ile Gly Ala Phe Ala Tyr Pro Phe Val Ser Asp
190                     20                  25                  30
191         Ala Leu Asn Asn Tyr Leu Asp Gln Gln Ile Ile Ala His Tyr Gln Ala
192                 35                  40                  45
193         Lys Ala Ser Gln Glu Asn Thr Lys Glu Met Ala Glu Leu Gln Glu Lys
194             50                  55                  60
```

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195         Met Glu Lys Lys Asn Gln Glu Leu Ala Lys Lys Gly Ser Asn Pro Gly
196         65                  70                  75                  80
197         Leu Asp Pro Phe Ser Glu Thr Gln Lys Thr Thr Lys Lys Pro Asp Lys
198                         85                  90                  95
199         Ser Tyr Phe Glu Ser His Thr Ile Gly Val Leu Thr Ile Pro Lys Ile
200                     100                 105                 110
201         Asn Val Arg Leu Pro Ile Phe Asp Lys Thr Asn Ala Leu Leu Leu Glu
202                 115                 120                 125
203         Lys Gly Ser Ser Leu Leu Glu Gly Thr Ser Tyr Pro Thr Gly Gly Thr
204             130                 135                 140
205         Asn Thr His Ala Val Ile Ser Gly His Arg Gly Leu Pro Gln Ala Lys
206         145                 150                 155                 160
207         Leu Phe Thr Asp Leu Pro Glu Leu Lys Lys Gly Asp Glu Phe Tyr Ile
208                         165                 170                 175
209         Glu Val Asn Gly Lys Thr Leu Ala Tyr Gln Val Asp Gln Ile Lys Thr
210                     180                 185                 190
211         Val Glu Pro Thr Asp Thr Lys Asp Leu His Ile Glu Ser Gly Gln Asp
212                 195                 200                 205
213         Leu Val Thr Leu Leu Thr Cys Thr Pro Tyr Met Ile Asn Ser His Arg
214             210                 215                 220
215         Leu Leu Val Arg Gly His Arg Ile Pro Tyr Gln Pro Glu Lys Ala Ala
216         225                 230                 235                 240
217         Ala Gly Met Lys Lys Val Ala Gln Gln Gln Asn Leu Leu Leu Trp Thr
218                         245                 250                 255
219         Leu Leu Leu Ile Ala Cys Ala Leu Ile Ile Ser Gly Phe Ile Ile Trp
220                     260                 265                 270
221         Tyr Lys Arg Arg Lys Lys Thr Thr Arg Lys Pro Lys
222                 275                 280
223   <210> SEQ ID NO 7
224   <211> LENGTH: 246
225   <212> TYPE: PRT
226   <213> ORGANISM: Streptococcus mutans
227   <400> SEQUENCE: 7
228         Met Lys Lys Glu Arg Gln Ser Arg Lys Lys Arg Ser Phe Leu Arg Thr
229          1               5                  10                  15
230         Phe Leu Pro Ile Leu Leu Leu Val Ile Gly Leu Ala Leu Ile Phe Asn
231                     20                  25                  30
232         Thr Pro Ile Arg Asn Ala Leu Ile Ala Trp Asn Thr Asn Arg Tyr Gln
233                 35                  40                  45
234         Val Ser Asn Val Ser Lys Lys Asp Ile Glu His Asn Lys Ala Ala His
235             50                  55                  60
236         Ser Ser Phe Asp Phe Lys Lys Val Glu Ser Ile Ser Thr Gln Ser Val
237         65                  70                  75                  80
238         Leu Ala Ala Gln Met Ala Ala Gln Lys Leu Pro Val Ile Gly Gly Ile
239                         85                  90                  95
240         Ala Ile Pro Asp Leu Lys Ile Asn Leu Pro Ile Phe Lys Gly Leu Asp
241                     100                 105                 110
242         Asn Val Gly Leu Thr Tyr Gly Ala Gly Thr Met Lys Asn Asp Gln Val
243                 115                 120                 125
244         Met Gly Glu Asn Asn Tyr Ala Leu Ala Ser His His Val Phe Gly Met
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VERIFICATION SUMMARY
PATENT APPLICATION **US/09/292,436**

Input Set: **I292436.RAW**

Line	?	Error/Warning	Original Text
16	W	"N" or "Xaa" used: Feature required	Leu Pro Xaa Thr Gly
63	W	Line data has been corrected	Val Trp Glu Lys Arg Lys Ile Phe Val Ala T

CORRECTION SUMMARY
PATENT APPLICATION **US/09/292,436**

Input Set: **I292436.RAW**

Line	Original Text	Corrected Data
63	Val Trp Glu Lys Arg Lys Ile Phe Val Ala T	Val Trp Glu Lys Arg Lys Ile Phe Val Ala T

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/292,437

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos — The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length — The rules require that a line not exceed 72 characters in length. This includes spaces. All text must be visible on page.

4 ____ Misaligned Amino Acid Numbering — The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

5 ____ Non-ASCII — This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.

7 ____ Wrong Designation — Sequence(s) ____ contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)

8 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES) — Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES) — Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)

13 ____ Patentin ver. 2.0 "bug" — Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.